PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Ian S. Zagon, et al. **Examiner:** R. Landsman

Serial No.: 09/431,843 **Art Unit:** 1646

Filed: November 2, 1999 **Docket:** 13038

For: NOVEL NUCLEIC ACID MOLECULES ENCODING OPIOID GROWTH FACTOR RECEPTORS **Dated:** June 19, 2000

Assistant Commissioner for Patents
Washington, D.C. 20231

STATEMENT UNDER 37 C.F.R. § 1.821(f)

Sir:

I hereby state that the content of the substitute paper and computer readable copies of the Sequence Listing submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Frank S. DiGiglio
Registration No. 31,346

SCULLY, SCOTT, MURPHY & PRESSER
400 Garden City Plaza
Garden City, New York 11530
(516) 742-4343
FSD/XZ:ab

CERTIFICATE OF MAILING UNDER 37 C.F.R. §1.8(a)

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231 on June 19, 2000.

Dated: June 19, 2000

Michelle Spina

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Ian S. Zagon, et al.	**Examiner:**	R. Landsman
Serial No.:	09/431,843	**Art Unit:**	1646
Filed:	November 2, 1999	**Docket:**	13038
For:	NOVEL NUCLEIC ACID MOLECULES ENCODING OPIOID GROWTH FACTOR RECEPTORS	**Date:**	June 19, 2000

Assistant Commissioner for Patents
Washington, DC 20231

Response to Notice to Comply under 37 C.F.R.§ 1.821

Sir:

In response to the Office Communication dated May 19, 2000 and in accordance with the provisions in 37 C.F.R. §1.821, Applicants submit herewith a substitute paper and a substitute computer readable copy of the Sequence Listing, along with a Statement Under 37 C.F.R. § 1.821(f), stating that these copies are identical. A copy of the Notice to Comply is also

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CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, DC 20231 on June 19, 2000.

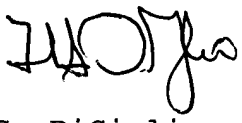
Dated: June 19 2000

Michelle Spina

F:\work\1123\13038\misc\13038.ntc2

enclosed. Applicants respectfully submit that the content of the paper and computer copies of the sequence listing does not introduce new matter.

Respectfully submitted,



Frank S. DiGiglio
Registration No. 31,346

SCULLY, SCOTT, MURPHY & PRESSER
400 Garden City Plaza
Garden City, New York 11530
(516) 742-4343

FSD/XZ:ab

Application No.: 09/431,341

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- [X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- [ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- [ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- [X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- [ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- [ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- [ ] 7. Other:

Applicant Must Provide:

- [X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- [X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- [X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

SEQUENCE LISTING

<110> Zagon S., Ian
Verderame, Michael
Allen, Sandra
McLaughlin J., Patricia

<120> NOVEL NUCLEIC ACID MOLECULES ENCODING OPIOID GROWTH FACTOR RECEPTORS

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Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
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Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
210 215 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225 230 235 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
245 250 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
260 265 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
290 295 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro Asp
305 310 315 320

His Glu Ala Ser Thr Gln Gly Arg Thr Cys Glu Pro Glu His Ser Lys
325 330 335

Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro Arg Ser Val Glu Pro
340 345 350

Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly Asp Glu Ala Gly Gly
355 360 365

His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro Lys Glu Ser Lys Lys
370 375 380

Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Gly Pro Gly
385 390 395 400

Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu Gly
405 410 415

Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val Gly
420 425 430

Gly Gln Asp Pro Gly Glu Ala Val Gln Pro Cys Arg Gln Pro Leu Gly
435 440 445

Ala Arg Val Ala Asp Lys Val Arg Lys Arg Arg Lys Val Asp Glu Gly
450 455 460

Thr Gly Asp Ser Ala Ala Val Ala Ser Gly Gly Ala Gln Thr Leu Ala
465 470 475 480

Leu Ala Gly Ser Pro Ala Pro Ser Gly His Pro Lys Ala Gly His Ser
485 490 495

Glu Asn Gly Val Glu Glu Asp Thr Glu Gly Arg Thr Gly Pro Lys Glu
500 505 510

Gly Thr Pro Gly Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
515 520 525

Pro Ala Gly Asp Glu Pro Ala Lys Thr Pro Ser Glu Thr Pro Gly Pro
530 535 540

Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Glu Ser Pro Ser Glu
545 550 555 560

Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu
565 570 575

Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp
580 585 590

Glu Pro Ala Lys Ile Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
595 600 605

Pro Thr Arg Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
610 615 620

Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
625 630 635 640

Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu
645 650 655

Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp
660 665 670

Glu Pro Ala Lys Ala Gly Glu Ala Ala Glu Leu Gln Asp Ala Glu Val
675 680 685

Glu Ser Ser Ala Lys Ser Gly Lys Pro
690 695

<210> 7
<211> 1601
<212> DNA
<213> Homo sapiens

<400> 7
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gccgccggcg cgagggacgc ggacgcaggg gacgaggacg aggagtcgga ggagccgcgg 180

gcggcgcggc ccagctcgtt ccagtccaga atgacagggt ccagaaactg gcgagccacg 240

agggacatgt gtaggtatcg gcacaactat ccggatctgg tggaacgaga ctgcaatggg 300

gacacgccaa acctgagttt ctacagaaat gagatccgct tcctgcccaa cggctgtttc 360

attgaggaca ttcttcagaa ctggacggac aactatgacc tccttgagga caatcactcc 420

tacatccagt ggctgtttcc tctgcgagaa ccaggagtga actggcatgc caagcccctc 480

acgctcaggg aggtcgaggt gtttaaaagc tcccaggaga tccaggagcg gcttgtccgg 540

gcctacgagc tcatgctggg cttctacggg atccggctgg aggaccgagg cacgggcacg 600

gtgggccgag cacagaacta ccagaagcgc ttccagaacc tgaactggcg cagccacaac 660

aacctccgca tcacacgcat cctcaagtcg ccgtgtgagc tgagcctcga gcacttccag 720

gcgccactgg tccgcttctt cctggaggag acgctggtgc ggcgggagct gccgggggtg 780

cggcagagtg ccctggacta cttcatgttc gccgtgcgct gccgacacca gcgccgccag 840

ctggtgcact tcgcctggga gcacttccgg ccccgctgca agttcgtctg ggggccccaa 900

gacaagctgc ggaggttcaa gcccagctct ctgccgcatc cgctcgaggg ctccaggaag 960

gtggaggagg aaggaagccc cggggacccc gaccacgagg ccagcaccca gggtcggacc 1020

tgtgggccag agcatagcaa gggtgggggc agggtggacg aggggcccca gccacggagc 1080

gtggagcccc aggatgcggg acccctggag aggagccagg gggatgaggc aggggccac 1140

ggggaagata ggccggagcc cttaagcccc aaagagagca agaagaggaa gctggagctg 1200

agccggcggg agcagccgcc cacagagcca ggccctcaga gtgcctcaga ggtggagaag 1260

atcgctctga atttggaggg gtgtgccctc agccagggca gcctcaggac ggggacccag 1320

gaagtgggcg gtcaggaccc tggggaggcc tcctgtccct gctgcagggg ctggggcctc 1380

cggagctgct gcgggctccc ctcaggctct gcttcgtgac ccgtgaccca tgacccacag 1440

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gcccctgtct ttgtaaattg acccttctgg agtgggggc g 1601

<210> 8
<211> 461
<212> PRT
<213> Homo sapiens

<400> 8

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Met Asp Asp Pro Asp Cys Asp Ser Thr Trp Glu Glu Asp Glu Glu Asp
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Ala Glu Asp Ala Glu Asp Glu Asp Cys Glu Asp Gly Glu Ala Ala Gly
             20                  25                  30

Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
         35                  40                  45

Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
     50                  55                  60

Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
 65                  70                  75                  80

Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
                 85                  90                  95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
            100                 105                 110

Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
        115                 120                 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
    130                 135                 140

His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
145                 150                 155                 160

Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
                165                 170                 175

Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
            180                 185                 190

Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
        195                 200                 205

Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
    210                 215                 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225                 230                 235                 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
                245                 250                 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
            260                 265                 270
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Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
290 295 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro Asp
305 310 315 320

His Glu Ala Ser Thr Gln Gly Arg Thr Cys Gly Pro Glu His Ser Lys
325 330 335

Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro Arg Ser Val Glu Pro
340 345 350

Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly Asp Glu Ala Gly Gly
355 360 365

His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro Lys Glu Ser Lys Lys
370 375 380

Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Glu Pro Gly
385 390 395 400

Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu Gly
405 410 415

Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val Gly
420 425 430

Gly Gln Asp Pro Gly Glu Ala Ser Cys Pro Cys Cys Arg Gly Trp Gly
435 440 445

Leu Arg Ser Cys Cys Gly Leu Pro Ser Gly Ser Ala Ser
450 455 460

<210> 9
<211> 2348
<212> DNA
<213> Homo sapiens

<400> 9
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tgggaggagg acgaggagga tgcggaggac gcggaggacg aggactgcga ggacggcgag 120

gccgccggcg cgagggacgc ggacgcaggg gacgaggacg aggagtcgga ggagccgcgg 180

gcggcgcggc ccagctcgtt ccagtccaga atgacagggt ccagaaactg gcgagccacg 240

agggacatgt gtaggtatcg gcacaactat ccggatctgg tggaacgaga ctgcaatggg 300

gacacgccaa acctgagttt ctacagaaat gagatccgct tcctgcccaa cggctgtttc 360

attgaggaca ttcttcagaa ctggacggac aactatgacc tccttgagga caatcactcc 420

tacatccagt ggctgtttcc tctgcgagaa ccaggagtga actggcatgc caagcccctc 480

acgctcaggg aggtcgaggt gtttaaaagc tcccaggaga tccaggagcg gcttgtccgg 540

gcctacgagc tcatgctggg cttctacggg atccggctgg aggaccgagg cacgggcacg 600

gtgggccgag cacagaacta ccagaagcgc ttccagaacc tgaactggcg cagccacaac 660

aacctccgca tcacacgcat cctcaagtcg ccgtgtgagc tgagcctcga gcacttccag 720

gcgccactgg tccgcttctt cctggaggag acgctggtgc ggcgggagct gccgggggtg 780

cggcagagtg ccctggacta cttcatgttc gccgtgcgct gccgacacca gcgccgccag 840

ctggtgcact tcgcctggga gcacttccgg ccccgctgca agttcgtctg ggggccccaa 900

gacaagctgc ggaggttcaa gcccagctct ctgccgcatc cgctcgaggg ctccaggaag 960

gtggaggagg aaggaagccc cggggacccc gaccacgagg ccagcaccca gggtcggacc 1020

tgtgggccag agcatagcaa gggtgggggc agggtggacg aggggcccca gccacggagc 1080

gtggagcccc aggatgcggg acccctggag aggagccagg gggatgaggc aggggccac 1140

ggggaagata ggccggagcc cttaagcccc aaagagagca agaagaggaa gctggagctg 1200

agccggcggg agcagccgcc cacagagcca ggccctcaga gtgcctcaga ggtggagaag 1260

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gaagtgggcg gtcaggaccc tggggaggca gtgcagccct gccgccaacc cctgggagcc 1380

agggtggccg acaaggtgag gaagcggagg aaggtggatg agggtgctgg ggacagtgct 1440

gcggtggcca gtggtggtgc ccagaccttg gcccttgccg ggtcccctgc cccatcgggg 1500

caccccaagg ctggacacag tgagaacggg gttgaggagg acacagaagg tcgaacgggg 1560

cccaaagaag gtacccctgg gagcccatcg gagaccccag gccccagccc agcaggacct 1620

gcaggggacg agccagccga gagcccatcg gagaccccag gcccccgccc agcaggacct 1680

gcaggggacg agccagccga gagcccatcg gagaccccag gcctccgccc ggcaggacct 1740

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gcaggggacg agccagccga gagcccatcg gagaccccag gcccccgccc ggcaggacct 1920

gcaggggacg aaccagccga gagcccatcg gagaccccag gccccagccc ggcaggacct 1980

acaagggatg agccagccaa ggcgggggag gcagcagagt tgcaggacgc agaggtggag 2040

tcttctgcca agtctgggaa gccttaagga aaggagtgcc cgtcggcgtc ttggtcctcc 2100

tgtccctgct gcaggggctg gggcctccgg agctgctgcg gactcccctc aggctctgct 2160

tcgtgacccg tgacccatga cccacagtgc tggcctcctg tggggccact atagcagcca 2220

ccagaagccg cgaggccctc agggaagccc aaggcctgca gaagcctcct ggcctggctg 2280

tgtcttcccc acccagctct cccctgcgcc cctgtctttg taaattgacc cttctggagt 2340

gggggggcg 2348

<210> 10
<211> 677
<212> PRT
<213> Homo sapiens

<400> 10

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Met Asp Asp Pro Asp Cys Asp Ser Thr Trp Glu Glu Asp Glu Glu Asp
  1               5                  10                  15

Ala Glu Asp Ala Glu Asp Glu Asp Cys Glu Asp Gly Glu Ala Ala Gly
             20                  25                  30

Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
         35                  40                  45

Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
     50                  55                  60

Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
 65                  70                  75                  80

Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
                 85                  90                  95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
            100                 105                 110

Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
        115                 120                 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
    130                 135                 140

His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
145                 150                 155                 160

Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
                165                 170                 175

Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
            180                 185                 190
```

Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
195 200 205

Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
210 215 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225 230 235 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
245 250 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
260 265 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
290 295 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro Asp
305 310 315 320

His Glu Ala Ser Thr Gln Gly Arg Thr Cys Gly Pro Glu His Ser Lys
325 330 335

Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro Arg Ser Val Glu Pro
340 345 350

Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly Asp Glu Ala Gly Gly
355 360 365

His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro Lys Glu Ser Lys Lys
370 375 380

Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Glu Pro Gly
385 390 395 400

Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu Gly
405 410 415

Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val Gly
420 425 430

Gly Gln Asp Pro Gly Glu Ala Val Gln Pro Cys Arg Gln Pro Leu Gly
435 440 445

Ala Arg Val Ala Asp Lys Val Arg Lys Arg Arg Lys Val Asp Glu Gly
450 455 460

Ala Gly Asp Ser Ala Ala Val Ala Ser Gly Gly Ala Gln Thr Leu Ala
465 470 475 480

Leu Ala Gly Ser Pro Ala Pro Ser Gly His Pro Lys Ala Gly His Ser
485 490 495

Glu Asn Gly Val Glu Glu Asp Thr Glu Gly Arg Thr Gly Pro Lys Glu
500 505 510

Gly Thr Pro Gly Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
515 520 525

Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
530 535 540

Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
545 550 555 560

Thr Pro Gly Leu Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu
565 570 575

Thr Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp
580 585 590

Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly
595 600 605

Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
610 615 620

Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
625 630 635 640

Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Lys
645 650 655

Ala Gly Glu Ala Ala Glu Leu Gln Asp Ala Glu Val Glu Ser Ser Ala
660 665 670

Lys Ser Gly Lys Pro
675

<210> 11
<211> 2289
<212> DNA
<213> Homo sapiens

<400> 11
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tgggaggagg acgaggagga tgcggaggac gcggaggacg aggactgcga ggacggcgag 120

gccgccggcg cgagggacgc ggacgcaggg gacgaggacg aggagtcgga ggagccgcgg 180

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gacacgccaa acctgagttt ctacagaaat gagatccgct tcctgcccaa cggctgtttc 360

attgaggaca ttcttcagaa ctggacggac aactatgacc tccttgagga caatcactcc 420

tacatccagt ggctgtttcc tctgcgagaa ccaggagtga actggcatgc caagcccctc 480

acgctcaggg aggtcgaggt gtttaaaagc tcccaggaga tccaggagcg gcttgtccgg 540

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gacaagctgc ggaggttcaa gcccagctct ctgccccatc cgctcgaggg ctccaggaag 960

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tgtgggccag agcatagcaa gggtgggggc agggtggacg aggggcccca gccacggagc 1080

gtggagcccc aggatgcggg acccctggag aggagccagg gggatgaggc aggggccac 1140

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agccggcggg agcagccgcc cacagagcca ggccctcaga gtgcctcaga ggtggagaag 1260

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gaagtgggcg gtcaggaccc tggggaggca gtgcagccct gccgccaacc cctgggagcc 1380

agggtggccg acaaggtgag gaagcggagg aaggtggatg agggtgctgg ggacagtgct 1440

gcggtggcca gtggtggtgc ccagaccttg gcccttgccg ggtcccctgc cccatcgggg 1500

caccccaagg ctggacacag tgagaacggg gttgaggagg acacagaagg tcgaacgggg 1560

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tcttctgcca agtctgggaa gccttaagga aaggagtgcc cgtcggcgtc ttggtcctcc 2040

tgtccctgct gcaggggctg gggcctccgg agctgctgcg ggctcccctc aggctctgct 2100

tcgtgacccg tgacccatga cccacagtgc tggcctcctg tggggccact atagcagcca 2160

ccagaagccg cgaggccctc agggaagccc aaggcctgca gaagcctcct ggcctggctg 2220

tgtcttcccc acccagctct cccctgcgcc cctgtctttg taaattgacc cttctggagt 2280

gggggggcgg 2289

<210> 12
<211> 657
<212> PRT
<213> Homo sapiens

<400> 12

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Met Asp Asp Pro Asp Cys Asp Ser Thr Trp Glu Glu Asp Glu Glu Asp
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             20                  25                  30

Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
         35                  40                  45

Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
     50                  55                  60

Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
 65                  70                  75                  80

Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
                 85                  90                  95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
            100                 105                 110

Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
        115                 120                 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
    130                 135                 140

His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
145                 150                 155                 160

Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
                165                 170                 175

Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
            180                 185                 190

Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
        195                 200                 205
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Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
210 215 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225 230 235 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
245 250 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
260 265 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
290 295 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro Asp
305 310 315 320

His Glu Ala Ser Thr Gln Gly Arg Thr Cys Gly Pro Glu His Ser Lys
325 330 335

Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro Arg Ser Val Glu Pro
340 345 350

Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly Asp Glu Ala Gly Gly
355 360 365

His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro Lys Glu Ser Lys Lys
370 375 380

Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Glu Pro Gly
385 390 395 400

Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu Gly
405 410 415

Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val Gly
420 425 430

Gly Gln Asp Pro Gly Glu Ala Val Gln Pro Cys Arg Gln Pro Leu Gly
435 440 445

Ala Arg Val Ala Asp Lys Val Arg Lys Arg Arg Lys Val Asp Glu Gly
450 455 460

Ala Gly Asp Ser Ala Ala Val Ala Ser Gly Gly Ala Gln Thr Leu Ala
465 470 475 480

Leu Ala Gly Ser Pro Ala Pro Ser Gly His Pro Lys Ala Gly His Ser
485 490 495

Glu Asn Gly Val Glu Glu Asp Thr Glu Gly Arg Thr Gly Pro Lys Glu
500 505 510

Gly Thr Pro Gly Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
515 520 525

Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
530 535 540

Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
545 550 555 560

Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Glu
565 570 575

Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp
580 585 590

Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly
595 600 605

Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
610 615 620

Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Lys Ala Gly Glu Ala
625 630 635 640

Ala Glu Leu Gln Asp Ala Glu Val Glu Ser Ser Ala Lys Ser Gly Lys
645 650 655

Pro

<210> 13
<211> 1232
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (51)
<223> n is unsure

<400> 13
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ggccgccggc gcgagggacg cggacgcagg ggacgaggac gaggagtcgg aggagccgcg 180

ggcggcgcgg cccagctcgt tccagtccag aatgacaggg tccagaaact ggcgagccac 240

gagggacatg tgtaggtatc ggcacaacta tccggatctg gtggaacgag actgcaatgg 300

ggacacgcca aacctgagtt tctacagaaa tgagatccgc ttcctgccca acggctgttt 360

cattgaggac attcttcaga actggacgga caactatgac ctccttgagg acaatcactc 420

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cacgctcagg gaggtcgagg tgtttaaaag ctcccaggag atccaggagc ggcttgtccg 540

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Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
         35                  40                  45

Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
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Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
 65                  70                  75                  80

Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
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Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
            100                 105                 110
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Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
115 120 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
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His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
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Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
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Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
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Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
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Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
210 215 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
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Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
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Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
260 265 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
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Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Pro Ala Gly Asp Glu Pro
305 310 315 320

Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr
325 330 335

Arg Asp Glu Pro Ala Lys Ala Gly Glu Ala Glu Ala Cys Cys Leu Ala
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Val Ser Ser His Pro Ala Leu Pro Cys Ala Pro Val Phe Val Asn Arg
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